

SEQUENCE LISTING

5 <110> Porro, Danilo
 Sauer, Michael
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 Pro Pro Arg Pro Pro Pro Pro Ala Thr Ala Ser Glu Ala Gln
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35 Phe Arg Lys Tyr Ala Gly Tyr Ala Ala Leu Ala Ile Phe Ser Gly Val
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| | Gln Val Gly Ala His Gly Thr Gly Ala Arg Leu Pro Pro Ile Asp Glu | | | |
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| 10 | Gln Val Ile Ser Met Lys Leu Val Thr Pro Ala Lys Gly Thr Ile Glu | | | |
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| | Leu Ser Arg Glu Lys Asp Pro Glu Leu Phe His Leu Ala Arg Cys Gly | | | |
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| | Leu Gly Gly Leu Gly Val Val Ala Glu Val Thr Leu Gln Cys Val Ala | | | |
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| 35 | Lys Tyr Arg Val Gln Asp Ser Gly Lys Lys Ser Pro Asp Ser Ser Glu | | | |
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| 40 | Ala Leu Asp Pro Leu Asn Asp Val His Val Ala Lys Val Asn Gln Ala | | | |
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| 15 | Lys Asp Lys Glu Glu Leu Glu Ala Leu Gln Ala Arg Ile Arg Lys Arg | | | |
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Asn Ala Lys His Lys Lys Ala Gln Ile Phe Arg Tyr Ala Pro Leu Pro
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35 Glu Asp Leu His Thr Val Ser Asn Trp Ser Gly Thr His Glu Val Gln
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Gln Glu Tyr Gly Leu Thr Leu Gln Asn Phe Ala Ser Ile Arg Glu Gln
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Gln Ile Gly Gly Ile Ile Gln Val Gly Ala His Gly Thr Gly Ala Arg

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| | His Leu Ala Arg Cys Gly Leu Gly Gly Leu Gly Val Val Ala Glu Val | | |
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| | Asn Lys His Val Lys Tyr Leu Tyr Ile Pro Tyr Thr Asp Thr Val Val | | |
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| 30 | Thr Pro Asp Ser Arg Glu Pro Asp Ile Asn Glu Leu Ser Phe Thr Glu | | |
| | 370 | 375 | 380 |
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| | Gln Gln Trp Val Ser Glu Thr Cys Phe Pro Ala Gly Thr Leu Ala Lys | | |
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| | 450 | 455 | 460 |
| | Gln Lys Glu Ala Ile Pro Ala Pro Ser Pro Ile Glu Gln Arg Trp Thr | | |
| 50 | 465 | 470 | 475 |
| | 480 | | |
| | Gly Arg Ser Lys Ser Pro Met Ser Pro Ala Phe Ser Thr Ala Glu Glu | | |
| | 485 | 490 | 495 |
| 55 | Asp Ile Phe Ser Trp Val Gly Ile Ile Met Tyr Leu Pro Thr Ala Asp | | |
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| 10 | Ala Lys Ile Glu Ile Pro Lys Asp Lys Glu Glu Leu Glu Ala Leu Gln 545 | 550 | 555 |
| 15 | Glu Arg Leu Arg Lys Arg Phe Pro Val Asp Ala Tyr Asn Lys Ala Arg 565 | 570 | 575 |
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Asp Glu Trp Leu Val Asn Leu Asp Arg Leu Asp Lys Val Gln Lys Phe
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Val Glu Tyr Pro Glu Leu His Tyr Ala Asp Val Thr Val Asp Ala Gly
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30 Met Arg Leu Tyr Gln Leu Asn Glu Phe Leu Gly Ala Lys Gly Tyr Ser
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Ile Gln Asn Leu Gly Ser Ile Ser Glu Gln Ser Val Ala Gly Ile Ile
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Gln Tyr Val Asn Leu Thr Ile Val Asn Gly Lys Gly Glu Leu Lys Phe
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Gly Phe Asn Ile Lys Ser Thr Gln Glu Val Ile Thr Phe Glu Asn Leu
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Thr Thr Asp Ala Gln Asn Gly Pro Ala Lys Ser Trp Trp Gly Thr Lys
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40 Gly Ile Tyr Ser Ala Lys Pro Glu Arg Tyr Phe Gln Pro Ser Ser Ile
 20 25 30

Asp Glu Val Val Glu Leu Val Lys Ser Ala Arg Leu Ala Glu Lys Ser
 45 35 40 45

Leu Val Thr Val Gly Ser Gly His Ser Pro Ser Asn Met Cys Val Thr
 50 55 60

50 Asp Glu Trp Leu Val Asn Leu Asp Arg Leu Asp Lys Val Gln Lys Phe
 65 70 75 80

Val Glu Tyr Pro Glu Leu His Tyr Ala Asp Val Thr Val Asp Ala Gly
 85 90 95

55 Met Arg Leu Tyr Gln Leu Asn Glu Phe Leu Gly Ala Lys Gly Tyr Ser
 100 105 110

Ile Gln Asn Leu Gly Ser Ile Ser Glu Gln Ser Val Ala Gly Ile Ile
 115 120 125

5 Ser Thr Gly Ser His Gly Ser Ser Pro Tyr His Gly Leu Ile Ser Ser
 130 135 140

Gln Tyr Val Asn Leu Thr Ile Val Asn Gly Lys Gly Glu Leu Lys Phe
 145 150 155 160

10 Leu Asp Ala Glu Asn Asp Pro Glu Val Phe Lys Ala Ala Leu Leu Ser
 165 170 175

Val Gly Lys Ile Gly Ile Ile Val Ser Ala Thr Ile Arg Val Val Pro
 180 185 190

Gly Phe Asn Ile Lys Ser Thr Gln Glu Val Ile Thr Phe Glu Asn Leu
 195 200 205

20 Leu Lys Gln Trp Asp Thr Leu Trp Thr Ser Ser Glu Phe Ile Arg Val
 210 215 220

Trp Trp Tyr Pro Tyr Thr Arg Lys Cys Val Leu Trp Arg Gly Asn Lys
 225 230 235 240

25 Thr Thr Asp Ala Gln Asn Gly Pro Ala Lys Ser Trp Trp Gly Thr Lys
 245 250 255

Leu Gly Arg Phe Phe Tyr Glu Thr Leu Leu Trp Ile Ser Thr Lys Ile
 30 260 265 270

Tyr Ala Pro Leu Thr Pro Phe Val Glu Lys Phe Val Phe Asn Arg Gln
 275 280 285

35 Tyr Gly Lys Leu Glu Lys Ser Ser Thr Gly Asp Val Asn Val Thr Asp
 290 295 300

Ser Ile Ser Gly Phe Asn Met Asp Cys Leu Phe Ser Gln Phe Val Asp
 305 310 315 320

40 Glu Trp Gly Cys Pro Met Asp Asn Gly Leu Glu Val Leu Arg Ser Leu
 325 330 335

Asp His Ser Ile Ala Gln Ala Ala Ile Asn Lys Glu Phe Tyr Val His
 45 340 345 350

Val Pro Met Glu Val Arg Cys Ser Asn Thr Thr Leu Pro Ser Glu Pro
 355 360 365

50 Leu Asp Thr Ser Lys Arg Thr Asn Thr Ser Pro Gly Pro Val Tyr Gly
 370 375 380

Asn Val Cys Arg Pro Phe Leu Asp Asn Thr Pro Ser His Cys Arg Phe
 385 390 395 400

55 Ala Pro Leu Glu Asn Val Thr Asn Ser Gln Leu Thr Leu Tyr Ile Asn
 405 410 415

Pro Thr Ile Tyr Arg Pro Phe Gly Cys Asn Thr Pro Ile His Lys Trp
 420 425 430
 5 Phe Thr Leu Phe Glu Asn Thr Met Met Val Ala Gly Gly Lys Pro His
 435 440 445
 Trp Ala Lys Asn Phe Leu Gly Ser Thr Thr Leu Ala Ala Gly Pro Val
 450 455 460
 10 Lys Lys Asp Thr Asp Tyr Asp Asp Phe Glu Met Arg Gly Met Ala Leu
 465 470 475 480
 Lys Val Glu Glu Trp Tyr Gly Glu Asp Leu Lys Lys Phe Arg Lys Ile
 485 490 495
 15 Arg Lys Glu Gln Asp Pro Asp Asn Val Phe Leu Ala Asn Lys Gln Trp
 500 505 510
 20 Ala Ile Ile Asn Gly Ile Ile Asp Pro Ser Glu Leu Ser Asp
 515 520 525
 25 <210> 8
 <211> 2138
 <212> DNA
 <213> *Saccharomyces cerevisiae*
 30 <400> 8
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 aagagtgccca ggcttagctga aaaaagctta gtactgttg gttcgggcca ttctcctagt 180
 aacatgtgcg ttactgtatga atggctgtt aacttagaca gattggacaa agtacaaaag 240
 tttgttgaat atcctgagtt acattatgcc gatgtcacag ttgatgccgg tatgaggctt 300
 35 taccatgtatga atgaattttt ggggtcgaaaa ggttaactcta tccaaaattt aggctctatc 360
 tcagaacaaa gtgttgctgg cataaatctct actggtagtc atggttcctc accttatcac 420
 ggtttgatt ctcttcataa cgtaaaacctg actattgtt atggtaaggg cgaattgaag 480
 ttcttggatg ccgaaaacga tccagaagtc tttaaagctg cttaacttcc agttggaaaa 540
 atcggatataca ttgtctctgc tactatcagg gtgttcccg gcttcaatat taaatccact 600
 40 caagaagtga ttacttttga aaacctttt aagcaatggg ataccctatg gacttcatct 660
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 aaaactacag atgcccaaaa tggtccagcc aagtcatggt ggggtaccaa gctgggtaga 780
 tttttctacg aaactcttatt atggatctct accaaaaatct atgcgccatt aacccctatt 840
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 45 gttaatgtta ccgattctat cagcgattt aatatggact gtttggtttca acaatttgg 960
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 50 tttgctccgt tgaaaaatgt taccaacagt cagttgacgt tgtacataaa tcctaccatt 1260
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 55 caagatcccg ataatgtatt ctggccaaac aaacagtggg ctatcataaa tggtattata 1560
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aataactatt cctagctgcc tatcaaagac ttttttttga attagagctt ttttagtaatc 1740
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 cggtaatgtat tggtcgtata agcaaaaacg aaacatcgcc atggcataac gtagatccta 1860
 5 tctacaggga agttttaga aatcagatag aaatgtat ttgagtgcgt atatattgca 1920
 gtacttttt tctctctagg atttaagtat gtttagtatt aactcatatc acatttttc 1980
 tttgtaaaaaa gcaaccattc gcaacaatgt cgatagtaga gacatgcata tcgtttgaaa 2040
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 <211> 440
 <212> PRT
 <213> Rattus norvegicus

15 <400> 9
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20 Tyr Gly Cys Ser Pro Glu Val Tyr Tyr Gln Pro Thr Ser Val Glu Glu
 20 25 30

Val Arg Glu Val Leu Ala Leu Ala Arg Glu Gln Lys Lys Lys Val Lys
 35 40 45

25 Val Val Gly Gly His Ser Pro Ser Asp Ile Ala Cys Thr Asp Gly
 50 55 60

30 Phe Met Ile His Met Gly Lys Met Asn Arg Val Leu Gln Val Asp Lys
 65 70 75 80

Glu Lys Lys Gln Ile Thr Val Glu Ala Gly Ile Leu Leu Ala Asp Leu
 85 90 95

35 His Pro Gln Leu Asp Glu His Gly Leu Ala Met Ser Asn Leu Gly Ala
 100 105 110

Val Ser Asp Val Thr Val Ala Gly Val Ile Gly Ser Gly Thr His Asn
 115 120 125

40 Thr Gly Ile Lys His Gly Ile Leu Ala Thr Gln Val Val Ala Leu Thr
 130 135 140

45 Leu Met Thr Ala Asp Gly Glu Val Leu Glu Cys Ser Glu Ser Arg Asn
 145 150 155 160

Ala Asp Val Phe Gln Ala Ala Arg Val His Leu Gly Cys Leu Gly Ile
 165 170 175

50 Ile Leu Thr Val Thr Leu Gln Cys Val Pro Gln Phe Gln Leu Gln Glu
 180 185 190

Thr Ser Phe Pro Ser Thr Leu Lys Glu Val Leu Asp Asn Leu Asp Ser
 195 200 205

55 His Leu Lys Arg Ser Glu Tyr Phe Arg Phe Leu Trp Phe Pro His Thr
 210 215 220

Glu Asn Val Ser Ile Ile Tyr Gln Asp His Thr Asn Lys Ala Pro Ser
 225 230 235 240

5 Ser Ala Ser Asn Trp Phe Trp Asp Tyr Ala Ile Gly Phe Tyr Leu Leu
 245 250 255

Glu Phe Leu Leu Trp Thr Ser Thr Tyr Leu Pro Cys Leu Val Gly Trp
 10 260 265 270

Ile Asn Arg Phe Phe Trp Met Leu Phe Asn Cys Lys Lys Glu Ser
 275 280 285

Ser Asn Leu Ser His Lys Ile Phe Thr Tyr Glu Cys Arg Phe Lys Gln
 15 290 295 300

His Val Gln Asp Trp Ala Ile Pro Arg Glu Lys Thr Lys Glu Ala Leu
 305 310 315 320

20 Leu Glu Leu Lys Ala Met Leu Glu Ala His Pro Lys Val Val Ala His
 325 330 335

Tyr Pro Val Glu Val Arg Phe Thr Arg Gly Asp Asp Ile Leu Leu Ser
 25 340 345 350

Pro Cys Phe Gln Arg Asp Ser Cys Tyr Met Asn Ile Ile Met Tyr Arg
 355 360 365

30 Pro Tyr Gly Lys Asp Val Pro Arg Leu Asp Tyr Trp Leu Ala Tyr Glu
 370 375 380

Thr Ile Met Lys Lys Phe Gly Gly Arg Pro His Trp Ala Lys Ala His
 385 390 395 400

35 Asn Cys Thr Gln Lys Asp Phe Glu Glu Met Tyr Pro Thr Phe His Lys
 405 410 415

Phe Cys Asp Ile Arg Glu Lys Leu Asp Pro Thr Gly Met Phe Leu Asn
 40 420 425 430

Ser Tyr Leu Glu Lys Val Phe Tyr
 435 440

45 <210> 10
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 <212> DNA
 <213> Rattus norvegicus

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 tcagagaggt gctggccctg gcccgggagc agaagaagaa agtgaaggtg gtgggtggtg 180
 gccactcgcc ttcagacatt gcctgcactg acgtttcat gatccacatg ggcaagatga 240
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acggcatcct ggccactcag gtggtggccc tgaccctgat gacagctgat ggagaagtgc 480
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 5 ctgagtaett ccgccttc tgggttc tgcactgatc acactgagaa cgtcagcatc atctaccaag 720
 accacaccaa caaggcccccc tcctctgcat ctaactgggtt ttgggactat gccatcggt 780
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 10 gggagaagac caaggaggcc ctactggagc taaaggccat gctggaggcc caccggaa 1020
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 15 gaccccaactg ggcaaaaggcc cacaattgca cccagaagga ctttgaggaa atgtacccca 1260
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 20 ctgacccatc ctccctgacca caaagaaagg ctggctctg ggccgggtcc tctctgcctt 1500
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 25 cgatgccccca gagatgtctg ctggctctgg gcaagccatc attcaaacgg gtccaaacctg 1860
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<210> 11
 <211> 319
 <212> PRT
 35 <213> Arabidopsis thaliana

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40 Ser Ala Val Gly Phe Gly Ala Ser Pro Leu Gly Ser Val Phe Gly Pro
 20 25 30

Val Ala Glu Asp Asp Ala Val Ala Thr Val Arg Glu Ala Phe Arg Leu
 45 35 40 45

Gly Ile Asn Phe Phe Asp Thr Ser Pro Tyr Tyr Gly Gly Thr Leu Ser
 50 55 60

50 Glu Lys Met Leu Gly Lys Gly Leu Lys Ala Leu Gln Val Pro Arg Ser
 65 70 75 80

Asp Tyr Ile Val Ala Thr Lys Cys Gly Arg Tyr Lys Glu Gly Phe Asp
 85 90 95

55 Phe Ser Ala Glu Arg Val Arg Lys Ser Ile Asp Glu Ser Leu Glu Arg
 100 105 110

Leu Gln Leu Asp Tyr Val Asp Ile Leu His Cys His Asp Ile Glu Phe
 115 120 125
 5 Gly Ser Leu Asp Gln Ile Val Ser Glu Thr Ile Pro Ala Leu Gln Lys
 130 135 140
 10 Leu Lys Gln Glu Gly Lys Thr Arg Phe Ile Gly Ile Thr Gly Leu Pro
 145 150 155 160
 15 Leu Asp Ile Phe Thr Tyr Val Leu Asp Arg Val Pro Pro Gly Thr Val
 165 170 175
 20 Asp Val Ile Leu Ser Tyr Cys His Tyr Gly Val Asn Asp Ser Thr Leu
 180 185 190
 25 Leu Asp Leu Leu Pro Tyr Leu Lys Ser Lys Gly Val Gly Val Ile Ser
 195 200 205
 30 Ala Ser Pro Leu Ala Met Gly Leu Leu Thr Glu Gln Gly Pro Pro Glu
 210 215 220
 Trp His Pro Ala Ser Pro Glu Leu Lys Ser Ala Ser Lys Ala Ala Val
 225 230 235 240
 35 Ala His Cys Lys Ser Lys Gly Lys Lys Ile Thr Lys Leu Ala Leu Gln
 245 250 255
 40 Tyr Ser Leu Ala Asn Lys Glu Ile Ser Ser Val Leu Val Gly Met Ser
 260 265 270
 Ser Val Ser Gln Val Glu Glu Asn Val Ala Ala Val Thr Glu Leu Glu
 275 280 285
 45 Ser Leu Gly Met Asp Gln Glu Thr Leu Ser Glu Val Glu Ala Ile Leu
 290 295 300
 Glu Pro Val Lys Asn Leu Thr Trp Pro Ser Gly Ile His Gln Asn
 305 310 315
 50 <210> 12
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 55 <213> Arabidopsis thaliana
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 accgtgcgcg aggcttccg tctcggtatc aacttctcg acacccccc gtattatgga 180
 ggaacactgt ctgagaaaat gcttggtaag ggactaaagg ctttgcagaat ccctagaatgt 240
 gactacattg tggctactaa gtgtggtaa tataaagaag gttttgattt cagtgctgag 300
 agagtaagaa agagtttgcgagagcttgcgagggcttc agcttgatcata ttgtgacata 360
 cttcattgcc atgacattgc gttcggtct cttgtatcata ttgtgatcata aacaattcc 420
 gctcttcaga aactgaaaca agagggaaag acccggtca ttggtatcac tggcttccg 480
 ttagatattt tcacttatgt tcttgatcga gtgcctccag ggactgtcga tgtgatattg 540
 tcatactgtc attacggcgt taatgattcg acgttgctgg atttactacc ttacttgaag 600

agcaaagggtg tgggtgtat aagtgccttcc ccat tagcaa tgggcctcct tacagaacaa 660
 ggtcctccctg aatggcaccc tgcttcccct gagctaagt ctgc aagcaa agccgcagg 720
 gctcaactgca aatcaaaggaa caagaagatc acaaaggtag ctctgc aata cagtttagca 780
 aacaaggaga tttcgctcggt gttgggttggg atgagctctg tctcacaggt agaagaaaat 840
 gttgcagcag ttacagagct tgaaaggctg gggatggatc aagaaactct gtctgagg 900
 gaagctattc tcgagcctgt aaagaatctg acatggccaa gtggaatcca tcagaactaa 960

5 <210> 13
 10 <211> 18
 <212> PRT
 <213> Artificial Sequence

15 <220>
 <223> Description of Artificial Sequence: motif I of
 aldo-keto reductase superfamily

20 <400> 13
 Gly Xaa Arg Xaa Xaa Asp Xaa Ala Xaa Xaa Xaa Xaa Glu Xaa Xaa
 1 5 10 15

25 Xaa Gly

30 <210> 14
 <211> 30
 <212> DNA
 <213> Artificial Sequence

35 <220>
 <223> Description of Artificial Sequence: Forward PCR
 Primer for L-galactono-1,4-lactone dehydrogenase
 from A. thaliana

40 <400> 14
 caagaaggcc taaatgttcc gttacgctcc 30

45 <210> 15
 <211> 30
 <212> DNA
 <213> Artificial Sequence

50 <220>
 <223> Description of Artificial Sequence: Reverse PCR
 Primer for L-galactono-1,4-lactone dehydrogenase
 from A. thaliana

55 <400> 15
 atgggcctt aagcagtggt ggagactggg 30

60 <210> 16
 <211> 26
 <212> DNA
 <213> Artificial Sequence

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      )
      )

<220>
<223> Description of Artificial Sequence: Forward PCR
      Primer for L-gulono-1,4-lactone oxidase from R.
      norvegicus
5

<400> 16
tgaggggtca gggtggttg tttcca
26

10
<210> 17
<211> 28
<212> DNA
<213> Artificial Sequence

15
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      _Primer for L-gulono-1,4-lactone oxidase from R.
      ~norvegicus
20

<400> 17
tggaatcatg gtccatgggt acaaagg
28

25
<210> 18
<211> 22
<212> DNA
<213> Artificial Sequence

30
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<223> Description of Artificial Sequence: Forward PCR
      Primer for D-arabinono-1,4-lactone oxidase from S.
      cerevisiae

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22

40
<210> 19
<211> 22
<212> DNA
<213> Artificial Sequence

45
<220>
<223> Description of Artificial Sequence: Reverse PCR
      Primer for D-arabinono-1,4-lactone oxidase from S.
      cerevisiae

50
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22

55
<210> 20
<211> 344
<212> PRT
<213> Saccharomyces cerevisiae

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5 His Pro Lys Thr Thr Glu Ile Tyr Phe Ser Leu Asn Asn Gly Val Arg
 20 25 30

Ile Pro Ala Leu Gly Leu Gly Thr Ala Asn Pro His Glu Lys Leu Ala
 10 35 40 45

Glu Thr Lys Gln Ala Val Lys Ala Ala Ile Lys Ala Gly Tyr Arg His
 50 55 60

Ile Asp Thr Ala Trp Ala Tyr Glu Thr Glu Pro Phe Val Gly Glu Ala
 15 65 70 75 80

Ile Lys Glu Leu Leu Glu Asp Gly Ser Ile Lys Arg Glu Asp Leu Phe
 85 90 95

20 Ile Thr Thr Lys Val Trp Pro Val Leu Trp Asp Glu Val Asp Arg Ser
 100 105 110

Leu Asn Glu Ser Leu Lys Ala Leu Gly Leu Glu Tyr Val Asp Leu Leu
 25 115 120 125

Leu Gln His Trp Pro Leu Cys Phe Glu Lys Ile Lys Asp Pro Lys Gly
 130 135 140

Ile Ser Gly Leu Val Lys Thr Pro Val Asp Asp Ser Gly Lys Thr Met
 30 145 150 155 160

Tyr Ala Ala Asp Gly Asp Tyr Leu Glu Thr Tyr Lys Gln Leu Glu Lys
 165 170 175

35 Ile Tyr Leu Asp Pro Asn Asp His Arg Val Arg Ala Ile Gly Val Ser
 180 185 190

Asn Phe Ser Ile Glu Tyr Leu Glu Arg Leu Ile Lys Glu Cys Arg Val
 40 195 200 205

Lys Pro Thr Val Asn Gln Val Glu Thr His Pro His Leu Pro Gln Met
 210 215 220

Glu Leu Arg Lys Phe Cys Phe Met His Asp Ile Leu Leu Thr Ala Tyr
 45 225 230 235 240

Ser Pro Leu Gly Ser His Gly Ala Pro Asn Leu Lys Ile Pro Leu Val
 245 250 255

50 Lys Lys Leu Ala Glu Lys Tyr Asn Val Thr Gly Asn Asp Leu Leu Ile
 260 265 270

Ser Tyr His Ile Arg Gln Gly Thr Ile Val Ile Pro Arg Ser Leu Asn
 275 280 285

55 Pro Val Arg Ile Ser Ser Ser Ile Glu Phe Ala Ser Leu Thr Lys Asp
 290 295 300

Glu Leu Gln Glu Leu Asn Asp Phe Gly Glu Lys Tyr Pro Val Arg Phe
 305 310 315 320

5 Ile Asp Glu Pro Phe Ala Ala Ile Leu Pro Glu Phe Thr Gly Asn Gly
 325 330 335

Pro Asn Leu Asp Asn Leu Lys Tyr
 340

10

<210> 21
 <211> 1509
 <212> DNA
 15 <213> *Saccharomyces cerevisiae*

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 tcaataaaaa tattatagat cgcttaaaaa ctcgtttatt gccgattata aatccaccaa 120
 20 aagccgcctc acccttacct ccgcctggaa aaattataat atataaagtg agcctcgtaa 180
 tacaggggta aaaaggaaag agggggatat caagcatctg gacttatttg cactatctcc 240
 gccttcaatt gataaaaagcg tcttgattt aatcaactgc tatcatgtct tcttcagtag 300
 cctcaaccga aaacatagtc gaaaatatgt tgcatccaaa gactacagaa atatacttt 360
 cactcaacca tggtgttcgt atcccagcac tgggtttggg gacagcaaat cctcacgaaa 420
 25 agttagctga aacaaaacaa gccgtaaaag ctgcaatcaa agctggatac aggacatgg 480
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 aagatggatc tatcaaaagg gaggatctt tcataaccac aaaagtgtgg ccgggttctat 600
 gggacgaagt ggacagatca ttgaatgaat ctggaaaagc tttaggcttg gaatacgtcg 660
 30 acttgcttt gcaacattgg ccgcctatgtt ttgaaaagat taaggaccct aaggggatca 720
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 tgagagccat tggtgtctca aattttcca ttgagtattt ggaacgtctc attaaggaat 900
 gcagagttaa gccaacggtg aaccaagtgg aaactcaccc tcacttacca caaatggAAC 960
 35 taagaaagt ctgccttatg cacgacattc tggtaacagc atactcacca tttagttccc 1020
 atggcgcacc aaacttggaa atcccactag tggaaaagct tgccgaaaag tacaatgtca 1080
 cagggaaatga cttgtaatt tcttaccata ttgacaagg cactatcgta attccgagat 1140
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 tacaagagtt gaacgacttc ggtggaaaat acccagttagt attcatcgat gagccatttg 1260
 40 cagccatcct tccagagttt actggtaacg gaccaactt ggacaattta aagtattaag 1320
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 ataatatta 1509

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<210> 22
 <211> 23
 <212> DNA
 <213> Artificial Sequence

50 <220>
 <223> Description of Artificial Sequence: Forward PCR
 Primer for L-galactose dehydrogenase from A.
 thaliana

55 <400> 22
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5 <210> 23
<211> 24
<212> DNA
<213> Artificial Sequence

10 <220>
<223> Description of Artificial Sequence: Reverse PCR
Primer for L-galactose dehydrogenase from A.
thaliana

15 <400> 23
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20 <210> 24
<211> 24
<212> DNA
<213> Artificial Sequence

25 <220>
<223> Description of Artificial Sequence: Saccharomyces
cerevisiae

30 <400> 24
atgtcttctt cagtagccctc aacc 24

35 <210> 25
<211> 29
<212> DNA
<213> Artificial Sequence

40 <220>
<223> Description of Artificial Sequence: Reverse PCR
Primer for D-arabinose dehydrogenase from S.
cerevisiae

45 <400> 25
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aldo-keto reductase superfamily

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Gly Xaa Xaa Asn

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